

GENSCAN predicted genes in sequence contig45

0.0 1.0 2.0 3.0 4.0 5.0 6.0 7.0 8.0 9.0 10.0 kb



10.0 11.0 12.0 13.0 14.0 15.0 16.0 17.0 18.0 19.0 20.0 kb




20.0 21.0 22.0 23.0 24.0 25.0 26.0 27.0 28.0 29.0 30.0 kb





30.0 31.0 32.0 33.0 34.0 35 kb






Key:

 Initial
exon

 Internal
exon

 Terminal
exon

 Single-exon
gene

 Optimal exon
 Suboptimal exon